

Asn Tyr Arg Cys Thr Cys Phe Asp Gly Phe Met Leu Ala His Asp Gly			
110	115	120	
cat aat tgt ctt gat gtg gac gag tgc ctg gag aac aat ggc ggc tgc		497	
His Asn Cys Leu Asp Val Asp Glu Cys Leu Glu Asn Asn Gly Gly Cys			
125	130	135	
cag cat acc tgt gtc aac gtc atg ggg agc tat gag tgc tgc tgc aag		545	
Gln His Thr Cys Val Asn Val Met Gly Ser Tyr Glu Cys Cys Cys Lys			
140	145	150	155
gag ggg ttt ttc ctg agt gac aat cag cac acc tgc att cac cgc tcg		593	
Glu Gly Phe Leu Ser Asp Asn Gln His Thr Cys Ile His Arg Ser			
160	165	170	
gaa gag ggc ctg agc tgc atg aat aag gat cac gac ggc tgt agt cac atc		641	
Glu Glu Gly Leu Ser Cys Met Asn Lys Asp His Gly Cys Ser His Ile			
175	180	185	
tgc aag gag gcc cca agg ggc agc gtc gcc tgt gag tgc agg cct ggt		689	
Cys Lys Glu Ala Pro Arg Gly Ser Val Ala Cys Glu Cys Arg Pro Gly			
190	195	200	
ttt gag ctg gcc aag aac cag aga gac tgc atc ttg acc tgt aac cat		737	
Phe Glu Leu Ala Lys Asn Gln Arg Asp Cys Ile Leu Thr Cys Asn His			
205	210	215	
ggg aac ggt ggg tgc cag cac tcc tgt gac gat aca gcc gat ggc cca		785	
Gly Asn Gly Gly Cys Gln His Ser Cys Asp Asp Thr Ala Asp Gly Pro			
220	225	230	235
gag tgc agc tgc cat cca cag tac aag atg cac aca gat ggg agg agc		833	
Glu Cys Ser Cys His Pro Gln Tyr Lys Met His Thr Asp Gly Arg Ser			
240	245	250	
tgc ctt gag cga gag gac act gtc ctg gag gtg aca gag agc aac acc		881	
Cys Leu Glu Arg Glu Asp Thr Val Leu Glu Val Thr Glu Ser Asn Thr			
255	260	265	
aca tca gtg gtg gat ggg gat aaa cgg gtg aaa cgg cgg ctg ctc atg		929	
Thr Ser Val Val Asp Gly Asp Lys Arg Val Lys Arg Arg Leu Leu Met			
270	275	280	
gaa acg tgt gtc aac aat gga ggc tgt gac cgc acc tgt aag gat		977	
Glu Thr Cys Ala Val Asn Gln Gly Gly Cys Asp Arg Thr Cys Lys Asp			
285	290	295	
act tcg aca ggt gtc cac tgc agt tgt cct gtt gga ttc act ctc cag		1025	
Thr Ser Thr Gly Val His Cys Ser Cys Pro Val Gly Phe Thr Leu Gln			
300	305	310	315
ttg gat ggg aag aca tgt aaa gat att gat gag tgc cag acc cgc aat		1073	
Leu Asp Gly Lys Thr Cys Lys Asp Ile Asp Glu Cys Gln Thr Arg Asn			
320	325	330	
gga ggt tgt gat cat ttc tgc aaa aac atc gtg ggc agt ttt gac tgc		1121	
Gly Gly Cys Asp His Phe Cys Lys Asn Ile Val Gly Ser Phe Asp Cys			
335	340	345	
ggc tgc aag aaa gga ttt aaa tta tta aca gat gag aag tct tgc caa		1169	
Gly Cys Lys Lys Gly Phe Lys Leu Leu Thr Asp Glu Lys Ser Cys Gln			

350

355

360

gat gtg gat gag tgc tct ttg gat agg acc tgt gac cac agc tgc atc Asp Val Asp Glu Cys Ser Leu Asp Arg Thr Cys Asp His Ser Cys Ile 365 370 375		1217
aac cac cct ggc aca ttt gct tgt gct tgc aac cga ggg tac acc ctg Asn His Pro Gly Thr Phe Ala Cys Ala Cys Asn Arg Gly Tyr Thr Leu 380 385 390 395		1265
tat ggc ttc acc cac tgt gga gac acc aat gag tgc agc atc aac aac Tyr Gly Phe Thr His Cys Gly Asp Thr Asn Glu Cys Ser Ile Asn Asn 400 405 410		1313
gga ggc tgt cag cag gtc tgt gtg aac aca gtg ggc agc tat gaa tgc Gly Gly Cys Gln Gln Val Cys Val Asn Thr Val Gly Ser Tyr Glu Cys 415 420 425		1361
cag tgc cac cct ggg tac aag ctc cac tgg aat aaa aaa gac tgt gtg Gln Cys His Pro Gly Tyr Lys Leu His Trp Asn Lys Lys Asp Cys Val 430 435 440		1409
gaa gtg aag ggg ctc ctg ccc aca agt gtg tca ccc cgt gtg tcc ctg Glu Val Lys Gly Leu Leu Pro Thr Ser Val Ser Pro Arg Val Ser Leu 445 450 455		1457
cac tgc ggt aag agt ggt gga gga gac ggg tgc ttc ctc aga tgt cac His Cys Gly Lys Ser Gly Gly Asp Gly Cys Phe Leu Arg Cys His 460 465 470 475		1505
tct ggc att cac ctc tct tca gat gtc acc acc atc agg aca agt gta Ser Gly Ile His Leu Ser Ser Asp Val Thr Thr Ile Arg Thr Ser Val 480 485 490		1553
acc ttt aag cta aat gaa ggc aag tgt agt ttg aaa aat gct gag ctg Thr Phe Lys Leu Asn Glu Gly Lys Cys Ser Leu Lys Asn Ala Glu Leu 495 500 505		1601
ttt ccc gag ggt ctg cga cca gca cta cca gag aag cac agc tca gta Phe Pro Glu Gly Leu Arg Pro Ala Leu Pro Glu Lys His Ser Ser Val 510 515 520		1649
aaa gag agc ttc cgc tac gta aac ctt aca tgc agc tct ggc aag caa Lys Glu Ser Phe Arg Tyr Val Asn Leu Thr Cys Ser Ser Gly Lys Gln 525 530 535		1697
gtc cca gga gcc cct ggc cga cca agc acc cct aag gaa atg ttt atc Val Pro Gly Ala Pro Gly Arg Pro Ser Thr Pro Lys Glu Met Phe Ile 540 545 550 555		1745
act gtt gag ttt gag ctt gaa act aac caa aag gag gtg aca gct tct Thr Val Glu Phe Glu Leu Glu Thr Asn Gln Lys Glu Val Thr Ala Ser 560 565 570		1793
tgt gac ctg agc tgc atc gta aag cga acc gag aag cgg ctc cgt aaa Cys Asp Leu Ser Cys Ile Val Lys Arg Thr Glu Lys Arg Leu Arg Lys 575 580 585		1841
GCC ATC CGC ACG CTC AGA AAG GCC GTC CAC AGG GAG CAG TTT CAC CTC Ala Ile Arg Thr Leu Arg Lys Ala Val His Arg Glu Gln Phe His Leu 590 595 600		1889

cag ctc tca ggc atg aac ctc gac gtg gct aaa aag cct ccc aga aca Gln Leu Ser Gly Met Asn Leu Asp Val Ala Lys Lys Pro Pro Arg Thr 605 610 615	1937
tct gaa cgc cag gca gag tcc tgt gga gtg ggc cag ggt cat gca gaa Ser Glu Arg Gln Ala Glu Ser Cys Gly Val Gly Gln Gly His Ala Glu 620 625 630 635	1985
aac caa tgt gtc agt tgc agg gct ggg acc tat tat gat gga gca cga Asn Gln Cys Val Ser Cys Arg Ala Gly Thr Tyr Tyr Asp Gly Ala Arg 640 645 650	2033
gaa cgc tgc att tta tgt cca aat gga acc ttc caa aat gag gaa gga Glu Arg Cys Ile Leu Cys Pro Asn Gly Thr Phe Gln Asn Glu Glu Gly 655 660 665	2081
caa atg act tgt gaa cca tgc cca aca gca gga aat tct ggg gcc ctg Gln Met Thr Cys Glu Pro Cys Pro Arg Pro Gly Asn Ser Gly Ala Leu 670 675 680	2129
aag acc cca gaa gct tgg aat atg tct gaa tgt gga ggt ctg tgt tct Lys Thr Pro Glu Ala Trp Asn Met Ser Glu Cys Gly Leu Cys Gln 685 690 695	2177
cct ggt gaa tat tct gca gat ggc ttt gca cct tgc cag ctc tgt gec Pro Gly Glu Tyr Ser Ala Asp Gly Phe Ala Pro Cys Gln Leu Cys Ala 700 705 710 715	2225
ctg ggc acg ttc cag cct gaa gct ggt cga act tcc tgc ttc ccc tgt Leu Gly Thr Phe Gln Pro Glu Ala Gly Arg Thr Ser Cys Phe Pro Cys 720 725 730	2273
gga gga ggc ctt gcc acc aaa cat cag gga gct act tcc ttt cag gac Gly Gly Gly Leu Ala Thr Lys His Gln Gly Ala Thr Ser Phe Gln Asp 735 740 745	2321
tgt gaa acc aga gtt caa tgt tca cct gga cat ttc tac aac acc acc Cys Glu Thr Arg Val Gln Cys Ser Pro Gly His Phe Tyr Asn Thr Thr 750 755 760	2369
act cac cga tgt att cgt tgc cca gtg gga aca tac cag cct gaa ttt Thr His Arg Cys Ile Arg Cys Pro Val Gly Thr Tyr Gln Pro Glu Phe 765 770 775	2417
gga aaa aat aat tgt gtt tct tgc cca gga aat act acg act gac ttt Gly Lys Asn Asn Cys Val Ser Cys Pro Gly Asn Thr Thr Asp Phe 780 785 790 795	2465
gat ggc tcc aca aac ata acc cag tgt aaa aac aga aga tgg gga ggg Asp Gly Ser Thr Asn Ile Thr Gln Cys Lys Asn Arg Arg Cys Gly Gly 800 805 810	2513
gag ctg gga gat ttc act ggg tac att gaa tcc cca aac tac cca ggc Glu Leu Gly Asp Phe Thr Gly Tyr Ile Glu Ser Pro Asn Tyr Pro Gly 815 820 825	2561
aat tac cca gcc aac acc gag tgt acy tgg acc att aac cca ccc ccc Asn Tyr Pro Ala Asn Thr Glu Cys Thr Trp Thr Ile Asn Pro Pro Pro 830 835 840	2609

aag cgc cgc atc ctg atc gtg gtc cct gag atc ttc ctg ccc ata gag	2657
Lys Arg Arg Ile Leu Ile Val Val Pro Glu Ile Phe Leu Pro Ile Glu	
845 850 855	
gac gac tgt ggg gac tat ctg gtg atg cgg aaa acc tct tca tcc aat	2705
Asp Asp Cys Gly Asp Tyr Leu Val Met Arg Lys Thr Ser Ser Ser Asn	
860 865 870 875	
tct gtg aca aca tat gaa acc tgc cag acc tac gaa cgc ccc atc gcc	2753
Ser Val Thr Thr Tyr Glu Thr Cys Gln Thr Tyr Glu Arg Pro Ile Ala	
880 885 890	
ttc acc tcc agg tca aag aag ctg tgg att cag ttc aag tcc aat gaa	2801
Phe Thr Ser Arg Ser Lys Lys Leu Trp Ile Gln Phe Lys Ser Asn Glu	
895 900 905	
ggg aac agc gct aga ggg ttc cag gtc cca tac gtg aca tat gat gag	2849
Gly Asn Ser Ala Arg Gly Phe Gln Val Pro Tyr Val Thr Tyr Asp Glu	
910 915 920	
gac tac cag gaa ctc att gaa gac ata gtt cga gat ggc agg ctc tat	2897
Asp Tyr Gln Glu Leu Ile Glu Asp Ile Val Arg Asp Gly Arg Leu Tyr	
925 930 935	
gca tct gag aac cat gag gaa ata ctt aag gat aag aaa ctt atc aag	2945
Ala Ser Glu Asn His Gln Glu Ile Leu Lys Asp Lys Lys Leu Ile Lys	
940 945 950 955	
gct ctg ttt gat gtc ctg gcc cat ccc cag aac tat ttc aag tac aca	2993
Ala Leu Phe Asp Val Leu Ala His Pro Gln Asn Tyr Phe Lys Tyr Thr	
960 965 970	
gcc cag gag tcc cga gag atg ttt cca aga tcg ttc atc cga ttg cta	3041
Ala Gln Glu Ser Arg Glu Met Phe Pro Arg Ser Phe Ile Arg Leu Leu	
975 980 985	
cgt tcc aaa gtg tcc agg ttt ttg aga cct tac aaa tga ctcagccac	3090
Arg Ser Lys Val Ser Arg Phe Leu Arg Pro Tyr Lys	
990 995	
gtgccactca atacaatgt tctgtatag gggtgggg acagagctgt ctcccttctg	3150
catgtcagca cagtcggta ttgctgcctc ccgttatcgt gactcattag agttcaattt	3210
tttagataa tacagatatt ttggtaatt gaacttgggt ttctttccc agcatcggtt	3270
atgttagactg agaatggctt tgatggcat cagttctca ctgtgtggg cggatgtctt	3330
ggatagatca cgggctggct gagctggact ttggtcagcc taggtgagac tcacctgtcc	3390
ttctgggtc ttactccctcc tcaaggagtc ttagatggaa aggaggccac agaataagct	3450
gcttattctg aaaccttcagc ttctcttage cccggccctct ctaaggggagc cctctgcact	3510
cgtgtgcagg ctctgaccagc gcagaacagg caagaggaaa gggaggaga cccctgcagg	3570
ctccccccac ccacccctttag accttggggg actcagtttc tccacagcc tctccagcc	3630
gtgtgataca agtttgatcc caggaaacttg agttctaagc agtgctgtg aaaaaaaaaaa	3690
gcagaaagaa tttagaaataa ataaaaacta agcacccctg gagacat	3737

<210> 2
<211> 999
<212> PRT
<213> Homo sapiens

<400> 2

Met Gly Val Ala Gly Arg Asn Arg Pro Gly Ala Ala Trp Ala Val Leu
1 5 10 15

Leu Leu Leu Leu Leu Leu Pro Pro Leu Leu Leu Leu Ala Gly Ala Val
20 25 30

Pro Pro Gly Arg Gly Arg Ala Ala Gly Pro Gln Glu Asp Val Asp Glu
35 40 45

Cys Ala Gln Gly Leu Asp Asp Cys His Ala Asp Ala Leu Cys Gln Asn
50 55 60

Thr Pro Thr Ser Tyr Lys Cys Ser Cys Lys Pro Gly Tyr Gln Gly Glu
65 70 75 80

Gly Arg Gln Cys Glu Asp Ile Asp Glu Cys Gly Asn Glu Leu Asn Gly
85 90 95

Gly Cys Val His Asp Cys Leu Asn Ile Pro Gly Asn Tyr Arg Cys Thr
100 105 110

Cys Phe Asp Gly Phe Met Leu Ala His Asp Gly His Asn Cys Leu Asp
115 120 125

Val Asp Glu Cys Leu Glu Asn Asn Gly Gly Cys Gln His Thr Cys Val
130 135 140

Asn Val Met Gly Ser Tyr Glu Cys Cys Cys Lys Glu Gly Phe Phe Leu
145 150 155 160

Ser Asp Asn Gln His Thr Cys Ile His Arg Ser Glu Glu Gly Leu Ser
165 170 175

Cys Met Asn Lys Asp His Gly Cys Ser His Ile Cys Lys Glu Ala Pro
180 185 190

Arg Gly Ser Val Ala Cys Glu Cys Arg Pro Gly Phe Glu Leu Ala Lys
195 200 205

Asn Gln Arg Asp Cys Ile Leu Thr Cys Asn His Gly Asn Gly Gly Cys
210 215 220

Gln His Ser Cys Asp Asp Thr Ala Asp Gly Pro Glu Cys Ser Cys His
225 230 235 240

Pro Gln Tyr Lys Met His Thr Asp Gly Arg Ser Cys Leu Glu Arg Glu
245 250 255

Asp Thr Val Leu Glu Val Thr Glu Ser Asn Thr Thr Ser Val Val Asp
260 265 270

Gly Asp Lys Arg Val Lys Arg Arg Leu Leu Met Glu Thr Cys Ala Val
275 280 285

Asn Asn Gly Cys Asp Arg Thr Cys Lys Asp Thr Ser Thr Gly Val
290 295 300

His Cys Ser Cys Pro Val Gly Phe Thr Leu Gln Leu Asp Gly Lys Thr
305 310 315 320

Cys Lys Asp Ile Asp Glu Cys Gln Thr Arg Asn Gly Gly Cys Asp His
325 330 335

Phe Cys Lys Asn Ile Val Gly Ser Phe Asp Cys Gly Cys Lys Lys Gly
340 345 350

Phe Lys Leu Leu Thr Asp Glu Lys Ser Cys Gln Asp Val Asp Glu Cys
355 360 365

Ser Leu Asp Arg Thr Cys Asp His Ser Cys Ile Asn His Pro Gly Thr
370 375 380

Phe Ala Cys Ala Cys Asn Arg Gly Tyr Thr Leu Tyr Gly Phe Thr His
385 390 395 400

Cys Gly Asp Thr Asn Glu Cys Ser Ile Asn Asn Gly Gly Cys Gln Gln
405 410 415

Val Cys Val Asn Thr Val Gly Ser Tyr Glu Cys Gln Cys His Pro Gly
420 425 430

Tyr Lys Leu His Trp Asn Lys Lys Asp Cys Val Glu Val Lys Gly Leu
435 440 445

Leu Pro Thr Ser Val Ser Pro Arg Val Ser Leu His Cys Gly Lys Ser

450	455	460
Gly Gly Gly Asp Gly Cys Phe Leu Arg Cys His Ser Gly Ile His Leu		
465	470	475
Ser Ser Asp Val Thr Thr Ile Arg Thr Ser Val Thr Phe Lys Leu Asn		
485	490	495
Glu Gly Lys Cys Ser Leu Lys Asn Ala Glu Leu Phe Pro Glu Gly Leu		
500	505	510
Arg Pro Ala Leu Pro Glu Lys His Ser Ser Val Lys Glu Ser Phe Arg		
515	520	525
Tyr Val Asn Leu Thr Cys Ser Ser Gly Lys Gln Val Pro Gly Ala Pro		
530	535	540
Gly Arg Pro Ser Thr Pro Lys Glu Met Phe Ile Thr Val Glu Phe Glu		
545	550	555
Leu Glu Thr Asn Gln Lys Glu Val Thr Ala Ser Cys Asp Leu Ser Cys		
565	570	575
Ile Val Lys Arg Thr Glu Lys Arg Leu Arg Lys Ala Ile Arg Thr Leu		
580	585	590
Arg Lys Ala Val His Arg Glu Gln Phe His Leu Gln Leu Ser Gly Met		
595	600	605
Asn Leu Asp Val Ala Lys Lys Pro Pro Arg Thr Ser Glu Arg Gln Ala		
610	615	620
Glu Ser Cys Gly Val Gly Gln Gly His Ala Glu Asn Gln Cys Val Ser		
625	630	635
Cys Arg Ala Gly Thr Tyr Tyr Asp Gly Ala Arg Glu Arg Cys Ile Leu		
645	650	655
Cys Pro Asn Gly Thr Phe Gln Asn Glu Glu Gly Gln Met Thr Cys Glu		
660	665	670
Pro Cys Pro Arg Pro Gly Asn Ser Gly Ala Leu Lys Thr Pro Glu Ala		
675	680	685
Trp Asn Met Ser Glu Cys Gly Gly Leu Cys Gln Pro Gly Glu Tyr Ser		
690	695	700

Ala Asp Gly Phe Ala Pro Cys Gln Leu Cys Ala Leu Gly Thr Phe Gln
 705 710 715 720

Pro Glu Ala Gly Arg Thr Ser Cys Phe Pro Cys Gly Gly Leu Ala
 725 730 735

Thr Lys His Gln Gly Ala Thr Ser Phe Gln Asp Cys Glu Thr Arg Val
 740 745 750

Gln Cys Ser Pro Gly His Phe Tyr Asn Thr Thr His Arg Cys Ile
 755 760 765

Arg Cys Pro Val Gly Thr Tyr Gln Pro Glu Phe Gly Lys Asn Asn Cys
 770 775 780

Val Ser Cys Pro Gly Asn Thr Thr Asp Phe Asp Gly Ser Thr Asn
 785 790 795 800

Ile Thr Gln Cys Lys Asn Arg Arg Cys Gly Gly Glu Leu Gly Asp Phe
 805 810 815

Thr Gly Tyr Ile Glu Ser Pro Asn Tyr Pro Gly Asn Tyr Pro Ala Asn
 820 825 830

Thr Glu Cys Thr Trp Thr Ile Asn Pro Pro Pro Lys Arg Arg Ile Leu
 835 840 845

Ile Val Val Pro Glu Ile Phe Leu Pro Ile Glu Asp Asp Cys Gly Asp
 850 855 860

Tyr Leu Val Met Arg Lys Thr Ser Ser Ser Asn Ser Val Thr Thr Tyr
 865 870 875 880

Glu Thr Cys Gln Thr Tyr Glu Arg Pro Ile Ala Phe Thr Ser Arg Ser
 885 890 895

Lys Lys Leu Trp Ile Gln Phe Lys Ser Asn Glu Gly Asn Ser Ala Arg
 900 905 910

Gly Phe Gln Val Pro Tyr Val Thr Tyr Asp Glu Asp Tyr Gln Glu Leu
 915 920 925

Ile Glu Asp Ile Val Arg Asp Gly Arg Leu Tyr Ala Ser Glu Asn His
 930 935 940

Gln Glu Ile Leu Lys Asp Lys Lys Leu Ile Lys Ala Leu Phe Asp Val
945 950 955 960

Leu Ala His Pro Gln Asn Tyr Phe Lys Tyr Thr Ala Gln Glu Ser Arg
965 970 975

Glu Met Phe Pro Arg Ser Phe Ile Arg Leu Leu Arg Ser Lys Val Ser
980 985 990

Arg Phe Leu Arg Pro Tyr Lys
995

<210> 3
<211> 997
<212> PRT
<213> Mus sp.

<400> 3

Met Gly Val Ala Gly Cys Gly Arg Pro Arg Glu Ala Arg Ala Leu Leu
1 5 10 15

Leu Leu Leu Leu Leu Pro Pro Leu Leu Ala Ala Ala Val Pro Pro
20 25 30

Asp Arg Gly Leu Thr Asn Gly Pro Ser Glu Asp Val Asp Glu Cys Ala
35 40 45

Gln Gly Leu Asp Asp Cys His Ala Asp Ala Leu Cys Gln Asn Thr Pro
50 55 60

Thr Ser Tyr Lys Cys Ser Cys Lys Pro Gly Tyr Gln Gly Glu Gly Arg
65 70 75 80

Gln Cys Glu Asp Met Asp Glu Cys Asp Asn Thr Leu Asn Gly Gly Cys
85 90 95

Val His Asp Cys Leu Asn Ile Pro Gly Asn Tyr Arg Cys Thr Cys Phe
100 105 110

Asp Gly Phe Met Leu Ala His Asp Gly His Asn Cys Leu Asp Met Asp
115 120 125

Glu Cys Leu Glu Asn Asn Gly Gly Cys Gln His Ile Cys Thr Asn Val
130 135 140

Ile Gly Ser Tyr Glu Cys Arg Cys Lys Glu Gly Phe Phe Leu Ser Asp
145 150 155 160

Asn Gln His Thr Cys Ile His Arg Ser Glu Glu Gly Leu Ser Cys Met
165 170 175

Asn Lys Asp His Gly Cys Gly His Ile Cys Lys Glu Ala Pro Arg Gly
180 185 190

Ser Val Ala Cys Glu Cys Arg Pro Gly Phe Glu Leu Ala Lys Asn Gln

195	200	205
Lys Asp Cys Ile Leu Thr Cys Asn His Gly Asn Gly Gly Cys Gln His		
210	215	220
Ser Cys Glu Asp Thr Ala Glu Gly Pro Glu Cys Ser Cys His Pro Arg		
225	230	235
Tyr Arg Leu His Ala Asp Gly Arg Ser Cys Leu Glu Gln Glu Gly Thr		
245	250	255
Val Leu Glu Gly Thr Glu Ser Asn Ala Thr Ser Val Ala Asp Gly Asp		
260	265	270
Lys Arg Val Lys Arg Arg Leu Leu Met Glu Thr Cys Ala Val Asn Asn		
275	280	285
Gly Gly Cys Asp Arg Thr Cys Lys Asp Thr Ser Thr Gly Val His Cys		
290	295	300
Ser Cys Pro Thr Gly Phe Thr Leu Gln Val Asp Gly Lys Thr Cys Lys		
305	310	315
Asp Ile Asp Glu Cys Gln Thr Arg Asn Gly Gly Cys Asn His Phe Cys		
325	330	335
Lys Asn Thr Val Gly Ser Phe Asp Cys Ser Cys Lys Lys Gly Phe Lys		
340	345	350
Leu Leu Thr Asp Glu Lys Ser Cys Gln Asp Val Asp Glu Cys Ser Leu		
355	360	365
Glu Arg Thr Cys Asp His Ser Cys Ile Asn His Pro Gly Thr Phe Ile		
370	375	380
Cys Ala Cys Asn Pro Gly Tyr Thr Leu Tyr Ser Phe Thr His Cys Gly		
385	390	395
Asp Thr Asn Glu Cys Ser Val Asn Asn Gly Gly Cys Gln Gln Val Cys		
405	410	415
Ile Asn Thr Val Gly Ser Tyr Glu Cys Gln Cys His Pro Gly Phe Lys		
420	425	430
Leu His Trp Asn Lys Lys Asp Cys Val Glu Val Lys Gly Phe Pro Pro		
435	440	445
Thr Ser Met Thr Pro Arg Val Ser Leu His Cys Gly Lys Ser Gly Gly		
450	455	460
Gly Asp Arg Cys Phe Leu Arg Cys Arg Ser Gly Ile His Leu Ser Ser		
465	470	475
Asp Val Val Thr Val Arg Thr Ser Val Thr Phe Lys Leu Asn Glu Gly		
485	490	495
Lys Cys Ser Leu Gln Lys Ala Lys Leu Ser Pro Glu Gly Leu Arg Pro		
500	505	510
Ala Leu Pro Glu Arg His Ser Ser Val Lys Glu Ser Phe Gln Tyr Ala		
515	520	525

Asn Leu Thr Cys Ser Pro Gly Lys Gln Val Pro Gly Ala Leu Gly Arg
 530 535 540
 Leu Asn Ala Pro Lys Glu Met Phe Ile Thr Val Glu Phe Glu Arg Glu
 545 550 555 560
 Thr Tyr Glu Lys Glu Val Thr Ala Ser Cys Asn Leu Ser Cys Val Val
 565 570 575
 Lys Arg Thr Glu Lys Arg Leu Arg Lys Ala Leu Arg Thr Leu Lys Arg
 580 585 590
 Ala Ala His Arg Glu Gln Phe His Leu Gln Leu Ser Gly Met Asp Leu
 595 600 605
 Asp Met Ala Lys Thr Pro Ser Arg Val Ser Gly Gln His Glu Glu Thr
 610 615 620
 Cys Gly Val Gly Gln Gly His Glu Glu Ser Gln Cys Val Ser Cys Arg
 625 630 635 640
 Ala Gly Thr Tyr Tyr Asp Gly Ser Gln Glu Arg Cys Ile Leu Cys Pro
 645 650 655
 Asn Gly Thr Phe Gln Asn Glu Gly Gln Val Thr Cys Glu Pro Cys
 660 665 670
 Pro Arg Pro Glu Asn Leu Gly Ser Leu Lys Ile Ser Glu Ala Trp Asn
 675 680 685
 Val Ser Asp Cys Gly Gly Leu Cys Gln Pro Gly Glu Tyr Ser Ala Asn
 690 695 700
 Gly Phe Ala Pro Cys Gln Leu Cys Ala Leu Gly Thr Phe Gln Pro Asp
 705 710 715 720
 Val Gly Arg Thr Ser Cys Leu Ser Cys Gly Gly Leu Pro Thr Lys
 725 730 735
 His Leu Gly Ala Thr Ser Phe Gln Asp Cys Glu Thr Arg Val Gln Cys
 740 745 750
 Ser Pro Gly His Phe Tyr Asn Thr Thr Thr His Arg Cys Ile Arg Cys
 755 760 765
 Pro Leu Gly Thr Tyr Gln Pro Glu Phe Gly Lys Asn Asn Cys Val Ser
 770 775 780
 Cys Pro Gly Asn Thr Thr Asp Phe Asp Gly Ser Thr Asn Ile Thr
 785 790 795 800
 Gln Cys Lys Asn Arg Lys Cys Gly Gly Glu Leu Gly Asp Phe Thr Gly
 805 810 815
 Tyr Ile Glu Ser Pro Asn Tyr Pro Gly Asn Tyr Pro Ala Asn Ser Glu
 820 825 830
 Cys Thr Trp Thr Ile Asn Pro Pro Pro Lys Arg Arg Ile Leu Ile Val
 835 840 845

Val Pro Glu Ile Phe Leu Pro Ile Glu Asp Asp Cys Gly Asp Tyr Leu
850 855 860

Val Met Arg Lys Thr Ser Ser Ser Asn Ser Val Thr Thr Tyr Glu Thr
865 870 875 880

Cys Gln Thr Tyr Glu Arg Pro Ile Ala Phe Thr Ser Arg Ser Lys Lys
885 890 895

Leu Trp Ile Gln Phe Lys Ser Asn Glu Gly Asn Ser Ala Arg Gly Phe
900 905 910

Gln Val Pro Tyr Val Thr Tyr Asp Glu Asp Tyr Gln Glu Leu Ile Glu
915 920 925

Asp Ile Val Arg Asp Gly Arg Leu Tyr Ala Ser Glu Asn His Gln Glu
930 935 940

Ile Leu Lys Asp Lys Lys Leu Ile Lys Ala Leu Phe Asp Val Leu Ala
945 950 955 960

His Pro Gln Asn Tyr Phe Lys Tyr Thr Ala Gln Glu Ser Arg Glu Met
965 970 975

Phe Pro Arg Ser Phe Ile Arg Leu Leu Arg Ser Lys Val Ser Arg Phe
980 985 990

Leu Arg Pro Tyr Lys
995

<210> 4
<211> 5
<212> PRT
<213> Unknown

<220>
<223> Cytokine receptor extacellular motif found in many species.

<220>
<221> UNSURE
<222> (3)..(3)
<223> "Xaa" at position 3 can be any amino acid.

<400> 4

Trp Ser Xaa Trp Ser
1 5